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164416 WA
DATE: 11/13/2001
TIME: 15:21:11

TECH CENTER 1600/2900

DEC 18 2001

RECEIVED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/940,166

Input Set : N:\Crf3\RULE60\09940166.txt
Output Set: N:\CRF3\11132001\I940166.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:

(i) APPLICANT: Blank, Gregory S.
Narindray, Daljit S.
Zapata, Gerardo A.

(ii) TITLE OF INVENTION: Protein Recovery

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/940,166
(B) FILING DATE: 27-Aug-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/097,309
(B) FILING DATE: 1998-06-12

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Schwartz, Timothy R.
(B) REGISTRATION NUMBER: 32171
(C) REFERENCE/DOCKET NUMBER: P1105R1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-7467
(B) TELEFAX: 650/952-9881

44 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

53	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
54	1			5						10					15	
56	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	
57				20						25					30	
59	Glu	Tyr	Thr	Met	His	Trp	Met	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
60				35						40					45	
62	Glu	Trp	Val	Ala	Gly	Ile	Asn	Pro	Lys	Asn	Gly	Gly	Thr	Ser	His	
63				50						55					60	

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```

65 Asn Gln Arg Phe Met Asp Arg Phe Thr Ile Ser Val Asp Lys Ser
66          65          70          75
68 Thr Ser Thr Ala Tyr Met Gln Met Asn Ser Leu Arg Ala Glu Asp
69          80          85          90
71 Thr Ala Val Tyr Tyr Cys Ala Arg Trp Arg Gly Leu Asn Tyr Gly
72          95          100          105
74 Phe Asp Val Arg Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val
75          110          115          120
77 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
78          125          130          135
80 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
81          140          145          150
83 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
84          155          160          165
86 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
87          170          175          180
89 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
90          185          190          195
92 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
93          200          205          210
95 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
96          215          220          225
98 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
99          230          235          240

```

101 Leu

102 241

104 (2) INFORMATION FOR SEQ ID NO: 2:

106 (i) SEQUENCE CHARACTERISTICS:

107 (A) LENGTH: 214 amino acids

108 (B) TYPE: Amino Acid

109 (D) TOPOLOGY: Linear

111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

113 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
114 1          5          10          15
116 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn
117          20          25          30
119 Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
120          35          40          45
122 Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser
123          50          55          60
125 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
126          65          70          75
128 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
129          80          85          90
131 Gly Asn Thr Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
132          95          100          105
134 Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
135          110          115          120
137 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu

```

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138          125          130          135
140 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
141          140          145          150
143 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
144          155          160          165
146 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
147          170          175          180
149 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
150          185          190          195
152 Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
153          200          205          210
155 Arg Gly Glu Cys
156          214
158 (2) INFORMATION FOR SEQ ID NO: 3:
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 36 amino acids
162 (B) TYPE: Amino Acid
163 (D) TOPOLOGY: Linear
165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
167 Leu Gly Gly Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu
168 1 5 10 15
170 Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys
171 20 25 30
173 Lys Leu Val Gly Glu Arg
174 35 36
176 (2) INFORMATION FOR SEQ ID NO: 4:
178 (i) SEQUENCE CHARACTERISTICS:
179 (A) LENGTH: 7 amino acids
180 (B) TYPE: Amino Acid
181 (D) TOPOLOGY: Linear
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
W--> 185 Leu Xaa Xaa Xaa Xaa Xaa Xaa
186 1 5 7
188 (2) INFORMATION FOR SEQ ID NO: 5:
190 (i) SEQUENCE CHARACTERISTICS:
191 (A) LENGTH: 2143 base pairs
192 (B) TYPE: Nucleic Acid
193 (C) STRANDEDNESS: Single
194 (D) TOPOLOGY: Linear
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
199 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
201 TCATTGCTGA GTTGTTATTT AAGCTTTGGA GATTATCGTC ACTGCAATGC 100
203 TTCGCAATAT GCGCAAAAT GACCAACAGC GGTGATTGA TCAGGTAGAG 150
205 GGGGCGCTGT ACGAGGTAAA GCCCGATGCC AGCATTCCTG ACGACGATAC 200
207 GGAGCTGCTG CCGGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT 250
209 AAAAAGTTAA TCTTTTCAAC AGCTGTCATA AAGTTGTCAC GGCCGAGACT 300
211 TATAGTCGCT TTGTTTTTAT TTTTAAATGT ATTTGTAACT AGAATTCGAG 350
213 CTCGCCGGGG ATCCTCTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC 400
215 GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA 450

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```

217 CGCTGATATC CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG 500
219 GCGATAGGGT CACCATCACC TGTCGTGCCA GTCAGGACAT CAACAATTAT 550
221 CTGAACGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA 600
223 CTATACCTCC ACCCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGTTCTG 650
225 GTTCTGGGAC GGATTACACT CTGACCATCA GCAGTCTGCA ACCGGAGGAC 700
227 TTCGCAACTT ATTACTGTCA GCAAGGTAAT ACTCTGCCGC CGACGTTCCG 750
229 ACAGGGCAGC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT 800
231 TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT 850
233 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA 900
235 GGTGGATAAC GCCCTCCAAT CGGGTAACATC CCAGGAGAGT GTCACAGAGC 950
237 AGGACAGCAA GGACAGCACC TACAGCCTCA GCAGACCCT GACGCTGAGC 1000
239 AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA 1050
241 GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAG 1100
243 CTGATCCTCT ACGCCGACG CATCGTGGCG CTAGTACGCA AGTTCACGTA 1150
245 AAAACGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 1200
247 TCTTCTTGCA TCTATGTTCT TTTTCTCTAT TGCTACAAAC GCGTACGCTG 1250
249 AGGTTAGCT GGTGGAGTCT GCGGTGGCC TGGTGCAGCC AGGGGGCTCA 1300
251 CTCCGTTTGT CCTGTGCAAC TTCTGGCTAC ACCTTTACCG AATACACTAT 1350
253 GCACTGGATG CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGCAGGGA 1400
255 TTAATCCTAA AAACGGTGGT ACCAGCCACA ACCAGAGGTT CATGGACCGT 1450
257 TTCACTATAA GCGTAGATAA ATCCACCAGT ACAGCCTACA TGCAAATGAA 1500
259 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTATTGTGCT AGATGGCGAG 1550
261 GCCTGAACCTA CGGCTTTGAC GTCCGTTATT TTGACGTCTG GGGTCAAGGA 1600
263 ACCCTGGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CCGTCTTCCC 1650
265 CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT 1700
267 GCCTGGTCAA GGAATACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA 1750
269 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCCTC 1800
271 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG 1850
273 GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCAG CAACACCAAG 1900
275 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAACTC ACACATGCCC 1950
277 GCGTGCCCCA GCACCAGAAC TGCTGGGCGG CCGCATGAAA CAGCTAGAGG 2000
279 ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG 2050
281 GCAAGACTCA AAAAGCTTGT CGGGGAGCGC TAAGCATGCG ACGGCCCTAG 2100
283 AGTCCCTAAC GCTCGGTTGC CGCCGGGCGT TTTTATTGT TAA 2143

```

285 (2) INFORMATION FOR SEQ ID NO: 6:

287 (i) SEQUENCE CHARACTERISTICS:

288 (A) LENGTH: 237 amino acids

289 (B) TYPE: Amino Acid

290 (D) TOPOLOGY: Linear

292 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

294 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
295 -23 -20 -15 -10
297 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
298 -5 1 5
300 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
301 10 15 20
303 Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln
304 25 30 35
306 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser

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307	40	45	50
309	Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser		
310	55	60	65
312	Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp		
313	70	75	80
315	Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Pro Thr		
316	85	90	95
318	Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala		
319	100	105	110
321	Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser		
322	115	120	125
324	Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg		
325	130	135	140
327	Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly		
328	145	150	155
330	Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr		
331	160	165	170
333	Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu		
334	175	180	185
336	Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
337	190	195	200
339	Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
340	205	210	214
342	(2) INFORMATION FOR SEQ ID NO: 7:		
344	(i) SEQUENCE CHARACTERISTICS:		
345	(A) LENGTH: 300 amino acids		
346	(B) TYPE: Amino Acid		
347	(D) TOPOLOGY: Linear		
349	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:		
351	Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe		
352	-23	-20	-15
354	Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser		
355	-5	1	5
357	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys		
358	10	15	20
360	Ala Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Met His Trp Met		
361	25	30	35
363	Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Asn		
364	40	45	50
366	Pro Lys Asn Gly Gly Thr Ser His Asn Gln Arg Phe Met Asp Arg		
367	55	60	65
369	Phe Thr Ile Ser Val Asp Lys Ser Thr Ser Thr Ala Tyr Met Gln		
370	70	75	80
372	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
373	85	90	95
375	Arg Trp Arg Gly Leu Asn Tyr Gly Phe Asp Val Arg Tyr Phe Asp		
376	100	105	110
378	Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr		
379	115	120	125

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/940,166

DATE: 11/13/2001

TIME: 15:21:12

Input Set : N:\Crf3\RULE60\09940166.txt
Output Set: N:\CRF3\11132001\I940166.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4